

OSIRIS: Free Open-source STR Analysis Software

National Center for Biotechnology Information, NLM, NIH, Bethesda, MD George Riley, Robert Goor, and Douglas Hoffman https://www.ncbi.nlm.nih.gov/projects/SNP/osiris/



Using OSIRIS

www.ncbi.nlm.nih.gov/projects/SNP/osiris/

Downloads include the OSIRIS User's

Guide with a Tutorial. The program

Source code is in the NCBI GitHub

repository. Collaborators welcome.

Questions or feedback, please contact:

The OSIRIS program is a free

download on the home page:

includes demonstration data.

Open Source Collaboration

forensics@ncbi.nlm.nih.gov

OSIRIS

- Free public domain software
- Expert system validated
- Sample Analysis and QC
- Cross-platform
- Windows (XP/7/8/10)
- Mac OS X
- Displays
- Stacked graph
- Table
- Sample detail
- Pre-configured for 38 kits
- Customizable export
- Spreadsheet, LIMS, graphics
- Analyzes .hid and .fsa files
- Rapid analysis
- >200 sample/min

Current Users

- Cell line validation / authentication
- Bio Sample ID/fingerprinting
- Chimerism/Engraftment testing for stem cell transplants
- Kinship Analysis
- Biometric/Forensic ID

Standalone Graphical User Interface

- Multiplatform Graphical User Interface Windows / Mac
- Flexible data export:
 - CSV/TSV tables of alleles, peak heights, other metrics

Homozygote D21S11 needs acceptance (1)

 Time
 1661
 1932.42
 2775.74
 3249.4:
 MIX05case2_victim notices:
 RECOMMEND REAMP LESS (OSIRIS - EXPORT)

 Peak Area
 63952.1
 70671.3
 4354.59
 38557.4
 ONE OR MORE PEAKS HAVE LASER OFF-SCALE

4537 4995 1011 2862

- Subsets of samples analyzed

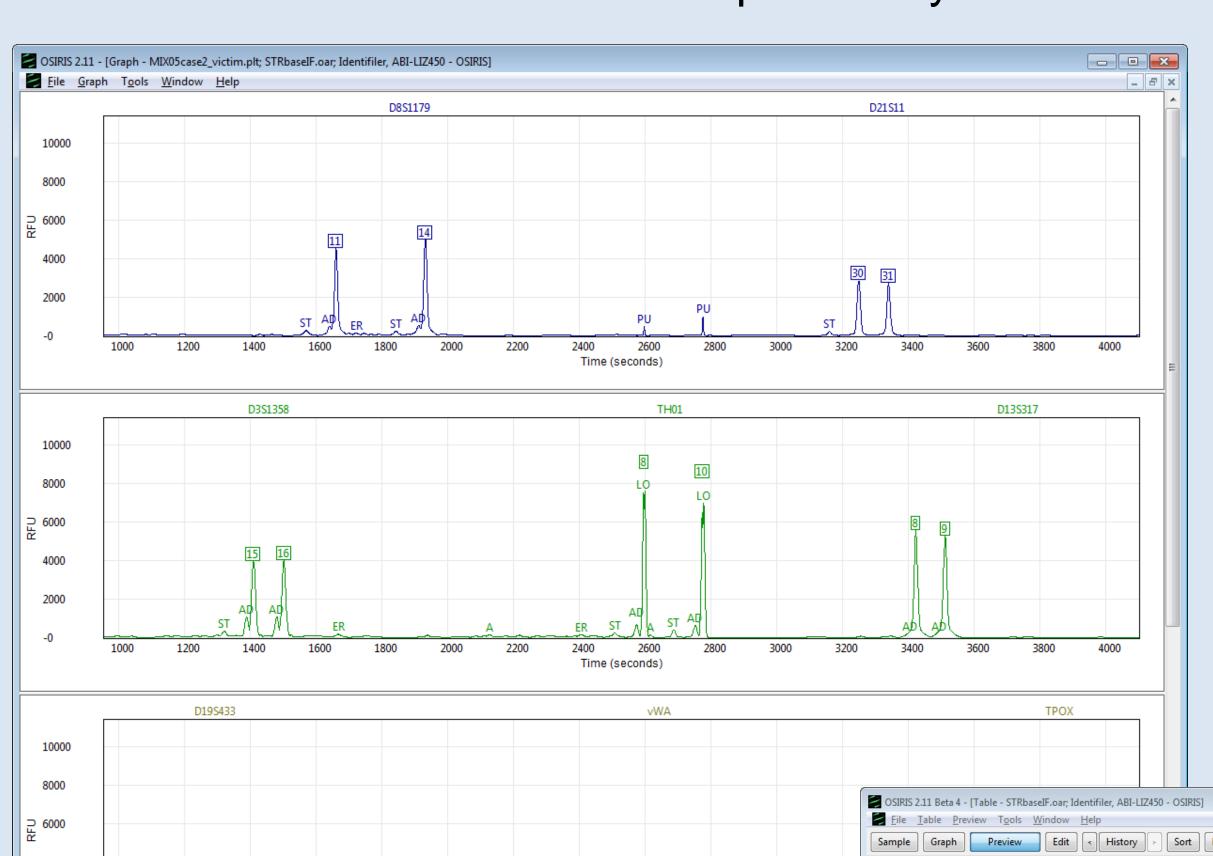


Table View

Adaptive locus color coding

Sort by name, severity, run time

Optional graphic locus preview

Graph view

- Flexible display labels
- Alleles, RFU, etc.
- Artifact-specific labels
- On-screen editing

OSIRIS Analysis

Identifies

- Alleles
- Artifacts

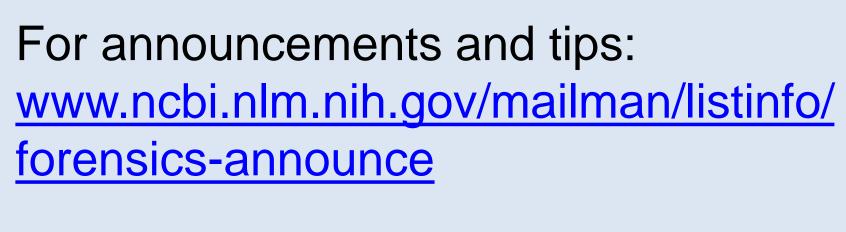
Uses novel quality metrics Novel peak and artifact signatures

Command Line Analysis

- Perform analysis without the user interface as part of an automated pipeline
- Multiplatform analysis module Windows / Mac / Unix -
- Written in C++ for exceptional performance
- Run-time parameters specified as simple name-value pairs
- Output files are in human and machine readable XML text

- Baseline
- Noise

Email a question





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Osiris Home page

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